AMENDMENTS TO THE CLAIMS

1. - 35. (canceled)

36. (currently amended) A method of determining whether a human has ~~identifying a human having~~ an increased risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) at ~~in said human's nucleic acids as represented by~~ position 101 of SEQ ID NO: 36673 or its complement, wherein at least one T allele at the SNP based on the sequence orientation of SEQ ID NO:36673 or at least one A allele at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 indicates said human has ~~is indicative of~~ an increased risk for developing said RF-positive rheumatoid arthritis ~~in said human~~.

37-38. (canceled)

39. (currently amended) The method of claim 36 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 10739 ~~1688~~.

40. (currently amended) The method of claim 39 ~~36~~ in which the SNP is located at position 42798 of SEQ ID NO: 10739.

41. (currently amended) The method of claim 36, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human ~~in which said human's nucleic acids are extracted from a biological sample therefrom~~.

42. (currently amended) The method of claim 41 in which said biological sample is blood, saliva, or buccal cells.

43. (currently amended) The method of claim 36, wherein said testing comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the determining step is carried out~~.

44. (currently amended) The method of claim 36, wherein said testing is performed ~~in which the identity of the SNP is determined by~~ using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

45. (currently amended) The method of claim 36, wherein said testing is performed using ~~in which the determining step is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification,~~ sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, ~~and~~ single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

46. (currently amended) A method of determining whether a human has ~~identifying a human having~~ a decreased risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) at ~~in said human's nucleic acids as represented by~~ position 101 of SEQ ID NO: 36673 or its complement, wherein a homozygous C/C genotype at the SNP based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 indicates said human has ~~is indicative of~~ a decreased risk for developing said RF-positive rheumatoid arthritis ~~in said human~~.

47-48. (canceled)

49. (previously presented) The method of claim 46 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 10739.

50. (currently amended) The method of claim 49 ~~46~~ in which the SNP is located at position 42798 of SEQ ID NO: 10739.

51. (currently amended) The method of claim 46, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human ~~in which said human's nucleic acids are extracted from a biological sample therefrom~~.

52. (currently amended) The method of claim 51 in which said biological sample is blood, saliva, or buccal cells.

53. (currently amended) The method of claim 46, wherein said testing comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the determining step is carried out~~.

54. (currently amended) The method of claim 46, wherein said testing is performed ~~in which the identity of the SNP is determined by~~ using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

55. (currently amended) The method of claim 46, wherein said testing is performed using ~~in which the determining step is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification,~~ sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, ~~and~~ single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

56. (currently amended) A method of determining a human's risk for developing RF-positive rheumatoid arthritis, comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) at ~~in said human's nucleic acids as represented by~~ position 101 of SEQ ID NO: 36673 or its complement, wherein at least one T allele at the SNP based on the sequence orientation of SEQ ID NO:36673 or at least one A allele at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 indicates said human has ~~is indicative of~~ an increased risk for developing said RF-positive rheumatoid arthritis ~~in said human~~, or a homozygous C/C genotype at the SNP based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 indicates said human has ~~is indicative of~~ a decreased risk for developing said RF-positive rheumatoid arthritis ~~in said human~~.

57-58. (canceled)

59. (previously presented) The method of claim 56 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 10739.

60. (currently amended) The method of claim 59 ~~56~~ in which the SNP is located at position 42798 of SEQ ID NO: 10739.

61. (currently amended) The method of claim 56, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human ~~in which said human's nucleic acids are extracted from a biological sample therefrom~~.

62. (currently amended) The method of claim 61 in which said biological sample is blood, saliva, or buccal cells.

63. (currently amended) The method of claim 56, wherein said testing comprises nucleic acid amplification ~~in which said human's nucleic acids are amplified before the determining step is carried out~~.

64. (currently amended) The method of claim 56, wherein said testing is performed ~~in which the identity of the SNP is determined by~~ using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

65. (currently amended) The method of claim 56, wherein said testing is performed using ~~in which the determining step is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification,~~ sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, ~~and~~ single-stranded conformation polymorphism, or denaturing gradient gel electrophoresis (DGGE).

66. (currently amended) The method of any one of claims 36, 46, and 56 ~~claim 56~~, further comprising providing a report of the identity of said SNP.

67. (currently amended) The method of any one of claims 36, 46, and 56 ~~claim 56~~, further comprising providing a report of said human's risk for developing RF-positive rheumatoid arthritis.

68. (previously presented) The method of claim 67, wherein the risk is an increased risk for developing RF-positive rheumatoid arthritis.

69. (previously presented) The method of claim 67, wherein the risk is a decreased risk for developing RF-positive rheumatoid arthritis.

70. (previously presented) The method of claim 67, wherein the report further shows the identity of said SNP.

71. (previously presented) The method of claim 70, wherein the identity of said SNP is at least one T allele based on the sequence orientation of SEQ ID NO:36673 or at least one A allele based on the sequence orientation of the complement of SEQ ID NO:36673, and wherein the report indicates said human has an increased risk for developing RF-positive rheumatoid arthritis.

72. (previously presented) The method of claim 70, wherein the identity of said SNP is a homozygous C/C genotype based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype based on the sequence orientation of the complement of SEQ ID NO:36673, and wherein the report indicates said human has a decreased risk for developing RF-positive rheumatoid arthritis.

73. (currently amended) The method of claim 66 ~~any one of claims 66-72~~, wherein the report is in paper form or computer readable medium form.

74. (new) The method of any one of claims 36, 46, and 56, wherein said testing is performed using an allele-specific method.

75. (new) The method of claim 74, wherein said allele-specific method is allele-specific probe hybridization, allele-specific primer extension, or allele-specific amplification.

76. (new) The method of claim 74, wherein said allele-specific method detects said T allele or said A allele.

77. (new) The method of any one of claims 41, 51, and 61, further comprising preparing said nucleic acid extract from said biological sample prior to said testing.

78. (new) The method of claim 77, further comprising obtaining said biological sample from said human prior to said preparing.

79. (new) The method of any one of claims 43, 53, and 63, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

80. (new) The method of claim 36, further comprising correlating the presence of said T allele or said A allele with an increased risk for RF-positive rheumatoid arthritis.

81. (new) The method of claim 46, further comprising correlating the presence of said homozygous C/C genotype or said homozygous G/G genotype with a decreased risk for RF-positive rheumatoid arthritis.

82. (new) The method of claim 56, further comprising correlating the presence of said T allele or said A allele with an increased risk for RF-positive rheumatoid arthritis, or correlating the presence of said homozygous C/C genotype or said homozygous G/G genotype with a decreased risk for RF-positive rheumatoid arthritis.

83. (new) The method of any one of claims 80, 81, and 82, wherein said correlating is performed by computer software.

84. (new) The method of any one of claims 36, 46, and 56 which is an automated method.

85. (new) The method of claim 67, wherein the report is in paper form or computer readable medium form.

86. (new) The method of claim 68, wherein the report is in paper form or computer readable medium form.

87. (new) The method of claim 69, wherein the report is in paper form or computer readable medium form.

88. (new) The method of claim 70, wherein the report is in paper form or computer readable medium form.

89. (new) The method of claim 71, wherein the report is in paper form or computer readable medium form.

90. (new) The method of claim 72, wherein the report is in paper form or computer readable medium form.